Amendments to the Claims:

Please cancel claim 67 and amend claims 55, 68, 70, 73, and 75. This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1.-54. (Cancelled)

55. (Currently Amended) A method of correlating gene and protein expression in a biological sample, the method comprising the steps of:

a) obtaining a biological sample;

b) generating a gene expression profile of the sample~~,~~;

c) ~~thereby~~ identifying a differentially expressed mRNA in the sample;

e~~d~~) determining the nucleotide sequence of the mRNA;

d~~e~~) predicting the amino acid sequence of the polypeptide encoded by the mRNA;

e~~f~~) predicting the mass of the encoded polypeptide;

f~~g~~) generating a protein profile of polypeptides in the sample by mass spectrometry; and

g~~h~~) determining the presence or absence in the protein profile of a polypeptide having a mass that correlates to the predicted mass of the encoded polypeptide, thereby correlating gene and protein expression in a biological sample.

56. (Previously Presented): The method of claim 55, wherein the biological sample comprises a cell lysate from a healthy cell.

57. (Previously Presented): The method of claim 55, wherein the biological sample comprises a cell lysate from a pathological cell.

58. (Previously Presented): The method of claim 55, wherein the biological sample comprises a cell lysate from a cell contacted by a toxic compound.

59. (Previously Presented): The method of claim 55, wherein the biological sample comprises a cell lysate from a cell of a subject who responds to a drug treatment.

60. (Previously Presented): The method of claim 55, wherein the biological sample comprises a cell lysate from a cell of a subject who does not respond to a drug treatment.

61. (Previously Presented): The method of claim 55, wherein the biological sample comprises a human cell.

62. (Previously Presented): The method of claim 55, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with a nucleic acid array.

63. (Previously Presented): The method of claim 55, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with an oligonucleotide array.

64. (Previously Presented): The method of claim 55, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with an mRNA array.

65. (Previously Presented): The method of claim 55, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with an EST array.

66. (Previously Presented): The method of claim 55, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with a northern blot or a dot blot.

67. (Cancelled)

68. (Currently Amended) The method of claim ~~67~~ 55, wherein the two biological samples are derived from a normal cell and a pathologic cell.

69. (Previously Presented): The method of claim 68, wherein the pathologic cell is a cancer cell.

70. (Currently Amended): The method of claim ~~67~~ 55, wherein the two biological samples are derived from a healthy cell and a cell exposed to a toxic compound.

71. (Previously Presented): The method of claim 55, wherein mass spectrometry is laser desorption/ionization mass spectrometry.

72. (Previously Presented): The method of claim 55, wherein mass spectrometry is electrospray mass spectrometry.

73. (Currently Amended): The method of claim 55, further comprising,

in step (d), after predicting the amino acid sequence of the polypeptide encoded by the mRNA, predicting a post-translational modification of the encoded polypeptide;

in step e), after predicting the mass of the encoded polypeptide, predicting the mass of the encoded polypeptide to reflect the post-translational modification; and

in step g), after determining the presence of absence in the protein profile of a polypeptide having a mass that correlates to the predicted mass of the encoded protein, determining the presence or absence of a polypeptide having a mass that correlates to the predicted mass of the encoded polypeptide having the post-translational modification.

74. (Previously Presented): The method of claim 73, wherein the post-translational modification is phosphorylation or glycosylation.

75. (Currently Amended): The method of claim 55 further comprising:

(i) after step (d), predicting at least one physio-chemical characteristic of the encoded polypeptide selected from the group consisting of isoelectric point, hydrophobicity, hydrophilicity, glycosylation, phosphorylation, epitope sequence, ligand binding sequence, and metal chelate binding;

(ii) fractionating the polypeptides in the sample according to the at least one physiochemical characteristic, retaining the fraction containing the predicted physiochemical proterty, and then ~~before~~ generating the protein profile of polypeptides in the sample by mass spectrometry in step (f); and

(iii) in step (g), correlating the predicted mass and the at least one physiochemical characteristic of the encoded polypeptide with a polypeptide in the protein expression profile.

76. (Previously Presented): The method of claim 75, wherein the physio-chemical characteristic is isoelectric point and fractionating the polypeptides comprises isoelectric focusing.

77. (Previously Presented): The method of claim 75, wherein the physiochemical characteristic is isoelectric point and fractionating the polypeptides comprises capturing polypeptides on a solid phase-bound ion exchange adsorbent, washing away unbound polypeptides and detecting the bound polypeptides by laser desoprtion/ionization mass spectrometry.

78. (Previously Presented): The method of claim 75, wherein the physiochemical characteristic is hydrophobicity and fractionating the polypeptides comprises capturing polypeptides on a solid phase-bound hydrophobic interaction adsorbent, washing away unbound polypeptides and detecting the bound polypeptides by laser desoprtion/ionization mass spectrometry.

79. (Previously Presented): The method of claim 75, wherein the physiochemical characteristic is hydrophilicity and fractionating the polypeptides comprises capturing polypeptides on a solid phase-bound hydrophilic interaction adsorbent, washing away unbound polypeptides and detecting the bound polypeptides by laser desoprtion/ionization mass spectrometry.

80. (Previously Presented): The method of claim 75, wherein the physiochemical characteristic is epitope sequence and fractionating the polypeptides comprises capturing

polypeptides on a solid phase-bound biospecific adsorbent, washing away unbound polypeptides and detecting the bound polypeptides by laser desoprtion/ionization mass spectrometry.

81. (Previously Presented): The method of claim 75, wherein the physiochemical characteristic is metal chelate binding and fractionating the polypeptides comprises capturing polypeptides on a solid phase-bound immobilized metal chelate adsorbent, washing away unbound polypeptides and detecting the bound polypeptides by laser desoprtion/ionization mass spectrometry.